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Impact of behavior on central and peripheral circadian clocks in the common vole *Microtus arvalis*, a mammal with ultradian rhythms

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Supporting Figure

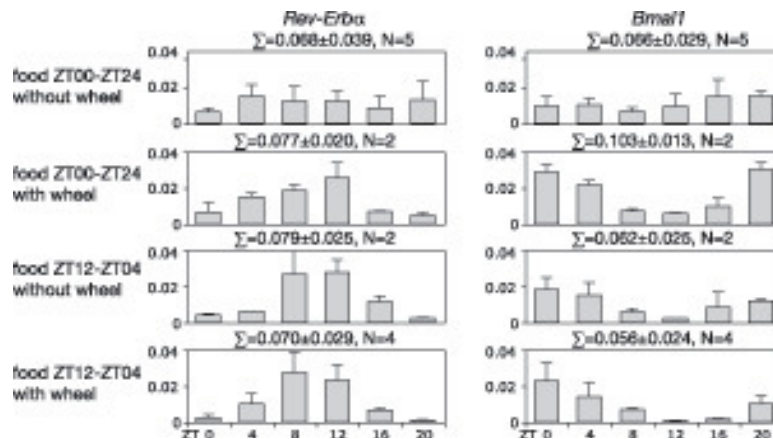


Fig. 6. Quantitative analysis of *Rev-erbα* and *Bmal1* transcripts. The graphs display the temporal accumulation of mRNAs as determined by TaqMan real-time RT-PCR using primers and TaqMan probes complementary to *Bmal1* and *Rev-erbα* mRNAs from voles. (*Inserts*) The sum of the values measured at six time intervals during the day (\pm SD) are given. Note that the mean values are similar, irrespective of whether the transcripts were expressed at nearly constitutive or strongly oscillating temporal patterns. To prepare primers and TaqMan probes for vole *Bmal1* and *Rev-erbα* mRNAs, cDNA sequences were amplified by RT-PCR, cloned, and sequenced. The resulting sequences have been submitted to GenBank and can be retrieved under accession nos. AM158956 and AM158957. TaqMan real-time RT-PCR experiments with vole liver RNAs were performed as described in ref. 1 by using the following primers and TaqMan probes: *Bmal1* primers, 5'-TGGACTGCAACCGCAAGAG-3'; 5'-GGTCATCTTTGTCTGTGTCCATACT-3'; *Bmal1* TaqMan probe: 5'-FAM-AGGGCAGCTCCACCGACTACCAGG-TAMRA-3'; *Rev-erbα* primers: 5'-GGTGGTAGAGTTTGCCAAGCA-3'; 5'-CTTCAGTAGGGTCACCTGGTCAT-3'; *Rev-erbα* TaqMan probe: 5'-FAM-CCGGCTTCCGTGACCTTTCCCA-TAMRA-3'. The TaqMan probes were designed based on sequences obtained with RT-PCR-amplified cDNA fragments from vole liver RNAs.

1. Gachon, F., Fonjallaz, P., Damiola, F., Gos, P., Kodama, T., Zakany, J., Duboule, D., Petit, B., Tafti, M. & Schibler, U. (2004) *Genes Dev.* **18**, 1397-1412.